

SEQUENCE LISTING

<110> WANG, XIAODONG
LIU, XUESONG

<120> DNA FRAGMENTATION FACTOR INVOLVED IN APOPTOSIS

<130> UTSD:546USD1

<140> UNKNOWN

<141> 2000-12-22

<150> 09/061,702

<151> 1998-04-16

<160> 21

<170> PatentIn Ver. 2.1

<210> 1

<211> 2839

<212> DNA

<213> Homo sapiens

<400> 1

ggcacccggc ctgtgccagc ttgcagagct caccagggtgc agacccctgc ggccagggcg 60
aggacggatc tgagcagctg ggcagcagggt gccaccgcct gtgggaccca gagggcttga 120
ggacatctgc aatgctccag aagcccaaga gcgtgaagct gcggggccctg cgccagccccga 180
ggaagttcgg cgtggctggc cggagctgcc aggaggtgct gcgcgaaggcg tgtctccgct 240
tccagctccc tgagcgcgggt tcccggtgt gcctgtacga ggatggcacc gagctgacgg 300
aagattactt ccccaagtgtt cccgacaacg ccgagctgggt gctgctcacc ttggggccagg 360
cctggcaggg ctatgtgagc gacatcaggg gcctcctcag tgcatttcac gagccacagg 420
tggggctcat ccaggccgccc cagcagctgc tgtgtatga gcaggccccca cagaggcaga 480
ggctgctggc tgacacctctg cacaacgtca gccagaacat cgccggccgag acccgggctg 540
aggacccggcc gtgggttgaa ggcttggagt cccgatttca gagcaagtct ggctatctga 600
gatacagctg tgagagccgg atccggagtt acctgaggaa ggtgagctcc tacccctcca 660
cagtggtgc ggaggctcag gaggaattcc tgcgggtcct cggctccatg tgccagaggc 720
tccggtccat gcagtaaat ggagactact tcgacagagg acccaaggcg ggcagccgcc 780
tctgcacacc ggaaggctgg ttctcctgcc agggccctt tgacatggac agctgcttat 840
caagacactc catcaacccc tacagtaaca gggagagcag gatectcttc agcacctgga 900
acctggatca cataatagaa aagaaacgcac ccatttcc tacactggtg gaagcaatta 960
aggaacacaaga tggaaagagaa gtggactggg agtattttt tggcctgctt tttacctcag 1020
agaacctaata actagtgcac attgtctgcc ataagaaaac cacccacaag ctcaactgtg 1080
acccgagcag aatctacaaa ccccaagacaa ggttgaagcg gaagcagccgt gtgcggaaac 1140
gccagtgaca cgtacacacc acgtcctgggt ctgttttga ggcctgacgt gggcatcatt 1200
ttaacaggtg ctttttttgt ttttttgggtt ttcgtttttt tggtcactcc agtagctcct 1260
ggaaaaaaacc ttaaaaaatg ttccctccaa atctgatttc attacatttc tgaattgttg 1320
ggttttttttt tgggtttttt tagatggagt ttcaacttttgc ttgcccaggc 1380

tggagtgtag tggcgcgatc tcggctcago ctcccgagta gctgggatta caggcatgtg 1440
ccaccacgcc cggtataatgt ttgttatttt agtagagacg gggtttcacc atgttggtca 1500
ggctggtctc aaactcctga cctcaggta tccgcccacc tcagcctccc aaagtgtgg 1560
gatgacaggt gtgagccact gcgcggcagcc tgaatcattt cttatacctt ctgacagccc 1620
aacttccaga ggacagctct ggggtactcg ttggatgtct gtgagtgacct ggtcatacgg 1680
gtcagtaggg ataagaattt tctctggct gaggaattct tctgttctct ggttccacca 1740
gcgttgggtt tgctcatgta atgtggcac catactaaa tgggtgtcatg gctgaagttg 1800
gcacacccgc ttgagggaca agttgttat gtatcagctc tctgtgggt ctcccttcc 1860
atggcaaattt ggcagctcca tcctcttgcat cttctaaatg cccaaaagag gtgtcatgct 1920
ttgggggtac gatgtttata ctccgtaaag aacatacaag gacattcaact gctgattttt 1980
ttttttgttt gttttagaca gggtctcaact ctgtcgctca ggctggagtg cagtgtatgca 2040
atcttggctc actgcaacct ccgcctctca ggttcaagtg gttctcctgc ctgcgcctcc 2100
caagtagctg ggattacagg cacctaccac cagggccagc taattttgtt atgttttagta 2160
gtaacggggtt ttcaccatgt tggccaggct gttctcgaac tcctgacctc aggtgatctg 2220
ccgcgcctcggt tctcccaaag tgctgggattt acaggcatga gccactgcac ctgcgcctgc 2280
gaattgttta taatggcaag aaataggaaa ccccccaatg tctgttgaac agctatcacc 2340
ttgaaccacg tgaaaactgct gtttcttagg ccaaaaatgg tgagcgatca tttatttcat 2400
gattcaacctt gatacattt catagtgcac aactgtgtca cagtttcagg cttttatgag 2460
gaaagcggtt ctgtgttagaa actggaagct gttcaggca tcggcagctg aaccctgc 2520
cggtggtcag cggtactatc atctcgatc atatggagct catgtcagcc gtgtgggtgg 2580
cggtgcaca gagacgtct ggaaggaaac acgcggatct gaacagcagt aatcctgggg 2640
gatacggggg ttgggctaga ttacagaggg ctcattttct acgtcatgta ttttatgata 2700
cttgaattttt ttgaaatggg catttattttt ataacatgtt aaaatgtact ttttaaatta 2760
agtcattttg taatatttga atttttacat ttgttgtaca atcaggaaaa gcaataaaga 2820
ttttcaaaaa ataaaaaaaaa 2839

<210> 2
<211> 338
<212> PRT
<213> Homo sapiens

<400> 2
Met Leu Gln Lys Pro Lys Ser Val Lys Leu Arg Ala Leu Arg Ser Pro
1 5 10 15

Arg Lys Phe Gly Val Ala Gly Arg Ser Cys Gln Glu Val Leu Arg Lys
20 25 30

Gly Cys Leu Arg Phe Gln Leu Pro Glu Arg Gly Ser Arg Leu Cys Leu
35 40 45

Tyr Glu Asp Gly Thr Glu Leu Thr Glu Asp Tyr Phe Pro Ser Val Pro
50 55 60

Asp Asn Ala Glu Leu Val Leu Leu Thr Leu Gly Gln Ala Trp Gln Gly
65 70 75 80

Tyr Val Ser Asp Ile Arg Arg Phe Leu Ser Ala Phe His Glu Pro Gln
85 90 95

Val Gly Leu Ile Gln Ala Ala Gln Gln Leu Leu Cys Asp Glu Gln Ala
100 105 110

Pro Gln Arg Gln Arg Leu Leu Ala Asp Leu Leu His Asn Val Ser Gln
115 120 125

Asn Ile Ala Ala Glu Thr Arg Ala Glu Asp Pro Pro Trp Phe Glu Gly
130 135 140

Leu Glu Ser Arg Phe Gln Ser Lys Ser Gly Tyr Leu Arg Tyr Ser Cys
145 150 155 160

Glu Ser Arg Ile Arg Ser Tyr Leu Arg Glu Val Ser Ser Tyr Pro Ser
165 170 175

Thr Val Gly Ala Glu Ala Gln Glu Glu Phe Leu Arg Val Leu Gly Ser
180 185 190

Met Cys Gln Arg Leu Arg Ser Met Gln Tyr Asn Gly Ser Tyr Phe Asp
195 200 205

Arg Gly Ala Lys Gly Ser Arg Leu Cys Thr Pro Glu Gly Trp Phe
210 215 220

Ser Cys Gln Gly Pro Phe Asp Met Asp Ser Cys Leu Ser Arg His Ser
225 230 235 240

Ile Asn Pro Tyr Ser Asn Arg Glu Ser Arg Ile Leu Phe Ser Thr Trp
245 250 255

Asn Leu Asp His Ile Ile Glu Lys Lys Arg Thr Ile Ile Pro Thr Leu
260 265 270

Val Glu Ala Ile Lys Glu Gln Asp Gly Arg Glu Val Asp Trp Glu Tyr
275 280 285

Phe Tyr Gly Leu Leu Phe Thr Ser Glu Asn Leu Lys Leu Val His Ile
290 295 300

Val Cys His Lys Lys Thr Thr His Lys Leu Asn Cys Asp Pro Ser Arg
305 310 315 320

Ile Tyr Lys Pro Gln Thr Arg Leu Lys Arg Lys Gln Pro Val Arg Lys
325 330 335

Arg Gln

<210> 3

<211> 1689

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (113)..(1105)

<400> 3

gcgtcgaccg aactacatct cccggcaggc tgcggaaggg ggtcgagtag aaggaccgcc 60

gctccggcct cccgcgactt ctgcgaagggtg ggcaggtccc accttgtgga gg atg gag 118
Met Glu

1

gtg acc ggg gac gcc ggg gta cca gaa tct ggc gag atc cgg act cta 166
Val Thr Gly Asp Ala Gly Val Pro Glu Ser Gly Glu Ile Arg Thr Leu
5 10 15

aag ccg tgt ctg ctg cgc aac tac agc cgc gaa cag cac ggc gtg 214
Lys Pro Cys Leu Leu Arg Arg Asn Tyr Ser Arg Glu Gln His Gly Val
20 25 30

gcc gcc tcc tgc ctc gaa gac ctg agg agc aag gcc tgt gac att ctg 262
Ala Ala Ser Cys Leu Glu Asp Leu Arg Ser Lys Ala Cys Asp Ile Leu
35 40 45 50

gcc att gat aag tcc ctg aca cca gtc acc ctt gtc ctg gca gag gat 310
Ala Ile Asp Lys Ser Leu Thr Pro Val Thr Leu Val Leu Ala Glu Asp
55 60 65

ggc acc ata gtg gat gat gac gat tac ttt ctg tgt cta cct tcc aat 358
Gly Thr Ile Val Asp Asp Asp Tyr Phe Leu Cys Leu Pro Ser Asn
70 75 80

act aag ttt gtg gca ttg gct agt aat gag aaa tgg gca tac aac aat 406
Thr Lys Phe Val Ala Leu Ala Ser Asn Glu Lys Trp Ala Tyr Asn Asn
85 90 95

tca gat gga ggt aca gct tgg att tcc caa gag tcc ttt gat gta gat 454
Ser Asp Gly Gly Thr Ala Trp Ile Ser Gln Glu Ser Phe Asp Val Asp
100 105 110

gaa aca gac agc ggg gca ggg ttg aag tgg aag aat gtg gcc agg gag			502
Glu Thr Asp Ser Gly Ala Gly Leu Lys Trp Lys Asn Val Ala Arg Glu			
115	120	125	130
ctg aaa gaa gat ctg tcc agc atc atc ctc cta tca gag gag gac ctc			550
Leu Lys Glu Asp Leu Ser Ser Ile Ile Leu Leu Ser Glu Glu Asp Leu			
135	140	145	
cag atg ctt gtt gac gct ccc tgc tca gac ctg gct cag gaa cta cgt			598
Gln Met Leu Val Asp Ala Pro Cys Ser Asp Leu Ala Gln Glu Leu Arg			
150	155	160	
cag agt tgt gcc acc gtc cag cgg ctg cag cac aca ctc caa cag gtg			646
Gln Ser Cys Ala Thr Val Gln Arg Leu Gln His Thr Leu Gln Gln Val			
165	170	175	
ctt gac caa aga gag gaa gtg cgt cag tcc aag cag ctc ctg cag ctg			694
Leu Asp Gln Arg Glu Glu Val Arg Gln Ser Lys Gln Leu Leu Gln Leu			
180	185	190	
tac ctc cag gct ttg gag aaa gag ggc agc ctc ttg tca aag cag gaa			742
Tyr Leu Gln Ala Leu Glu Lys Glu Gly Ser Leu Leu Ser Lys Gln Glu			
195	200	205	210
gag tcc aaa gct gcc ttt ggt gag gag gtg gat gca gta gac acg ggt			790
Glu Ser Lys Ala Ala Phe Gly Glu Glu Val Asp Ala Val Asp Thr Gly			
215	220	225	
atg agc aga gag acc tcc tcg gac gtt gcg ctg gcg agc cac atc ctt			838
Met Ser Arg Glu Thr Ser Ser Asp Val Ala Leu Ala Ser His Ile Leu			
230	235	240	
act gca ctg agg gag aag cag gct cca gag ctg agc tta tct agt cag			886
Thr Ala Leu Arg Glu Lys Gln Ala Pro Glu Leu Ser Leu Ser Ser Gln			
245	250	255	
gat ttg gag ttg gtt acc aag gaa gac ccc aaa gca ctg gct gtt gcc			934
Asp Leu Glu Leu Val Thr Lys Glu Asp Pro Lys Ala Leu Ala Val Ala			
260	265	270	
ttg aac tgg gac ata aag aag acg gag act gtt cag gag gcc tgt gag			982
Leu Asn Trp Asp Ile Lys Lys Thr Glu Thr Val Gln Glu Ala Cys Glu			
275	280	285	290
cgg gag ctc gcc ctg cgc ctg cag cag acg cag agc ttg cat tct ctc			1030
Arg Glu Leu Ala Leu Arg Leu Gln Gln Thr Gln Ser Leu His Ser Leu			
295	300	305	

cgg agc atc tca gca agc aag gcc tca cca cct ggt gac ctg cag aat 1078
Arg Ser Ile Ser Ala Ser Lys Ala Ser Pro Pro Gly Asp Leu Gln Asn
310 315 320

cct aag cga gcc aga cag qat ccc aca tagcagcagc ggaaagtgtg 1125
Pro Lys Arg Ala Arg Gln Asp Pro Thr
325 330

ccaaggaagc tctgtggcgt tgtgttattg gtagacaccc tcagcctcat catttgacta 1185
cctatgtact actctacccc ctgccttaga gcaccttcca gagaagctat tccaggtctc 1245
aacatacgcc gttccaccaa tttttttt agccccacca gtttcaggac ttctgccaat 1305
tttgaatgat atagctgcac caacaatatac ccgcctcctc taattacata tgatgttctc 1365
tgttcaaaag taattggcag tgattggcca ggcgcagtgg ctcacgcctg taatcccagc 1425
actgggaggc cgaggggggc ggatcgtgaa gtcaggagat cgagaccatc ctggctaaca 1485
tggtaaaacc ctgtctctac taaaaataca aaaaaaatta gccagccatg gtggcgggagc 1545
cctgtaatcc cagctacttg ggaggctgag gcaggagaat ggcatgaacc tgggaggcag 1605
agcttgcagt gagctgagat tgcgccactg cactccagcc tgggcaacag agcgagactc 1665
cgtctcaaaa aaaaaaaaaa aaaa 1689

<210> 4
<211> 331
<212> PRT
<213> Homo sapiens

<400> 4
Met Glu Val Thr Gly Asp Ala Gly Val Pro Glu Ser Gly Glu Ile Arg
1 5 10 15
Thr Leu Lys Pro Cys Leu Leu Arg Arg Asn Tyr Ser Arg Glu Gln His
20 25 30
Gly Val Ala Ala Ser Cys Leu Glu Asp Leu Arg Ser Lys Ala Cys Asp
35 40 45
Ile Leu Ala Ile Asp Lys Ser Leu Thr Pro Val Thr Leu Val Leu Ala
50 55 60
Glu Asp Gly Thr Ile Val Asp Asp Asp Tyr Phe Leu Cys Leu Pro

65 70 75 80

Ser Asn Thr Lys Phe Val Ala Leu Ala Ser Asn Glu Lys Trp Ala Tyr
 85 90 95

Asn Asn Ser Asp Gly Gly Thr Ala Trp Ile Ser Gln Glu Ser Phe Asp
 100 105 110

Val Asp Glu Thr Asp Ser Gly Ala Gly Leu Lys Trp Lys Asn Val Ala
 115 120 125

Arg Glu Leu Lys Glu Asp Leu Ser Ser Ile Ile Leu Leu Ser Glu Glu
 130 135 140

Asp Leu Gln Met Leu Val Asp Ala Pro Cys Ser Asp Leu Ala Gln Glu
 145 150 160

Leu Arg Gln Ser Cys Ala Thr Val Gln Arg Leu Gln His Thr Leu Gln
 165 170 175

Gln Val Leu Asp Gln Arg Glu Glu Val Arg Gln Ser Lys Gln Leu Leu
 180 185 190

Gln Leu Tyr Leu Gln Ala Leu Glu Lys Glu Gly Ser Leu Leu Ser Lys
 195 200 205

Gln Glu Glu Ser Lys Ala Ala Phe Gly Glu Glu Val Asp Ala Val Asp
 210 215 220

Thr Gly Met Ser Arg Glu Thr Ser Ser Asp Val Ala Leu Ala Ser His
 225 230 240

Ile Leu Thr Ala Leu Arg Glu Lys Gln Ala Pro Glu Leu Ser Leu Ser
 245 250 255

Ser Gln Asp Leu Glu Leu Val Thr Lys Glu Asp Pro Lys Ala Leu Ala
 260 265 270

Val Ala Leu Asn Trp Asp Ile Lys Lys Thr Glu Thr Val Gln Glu Ala
 275 280 285

Cys Glu Arg Glu Leu Ala Leu Arg Leu Gln Gln Thr Gln Ser Leu His
 290 295 300

Ser Leu Arg Ser Ile Ser Ala Ser Lys Ala Ser Pro Pro Gly Asp Leu
 305 310 315 320

Gln Asn Pro Lys Arg Ala Arg Gln Asp Pro Thr

325

330

<210> 5
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (6)..(12)
<223> N = Inosine

<220>
<221> modified_base
<222> (11)..(15)
<223> R = A or G

<220>
<221> modified_base
<222> (18)..(24)
<223> Y = C or T

<220>
<221> modified_base
<222> (10)
<223> W = A or T

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 5
gaggtnganw rngartaytt ytaggg

26

<210> 6
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 6
attttaggtga cactatagaa

20

TESTCASES

<210> 7
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (3)
<223> R = A or G

<220>
<221> modified_base
<222> (6)..(24)
<223> Y = C or T

<220>
<221> modified_base
<222> (15)..(21)
<223> N = Inosine

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 7
gartaytttyt ayggnytnyt nttyac

26

<210> 8
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (3)..(9)
<223> Y = C or T

<220>
<221> modified_base
<222> (6)
<223> N = A, C, G or T

<220>
<221> modified_base
<222> (12)

<223> R = A or G	
<220>	
<221> modified_base	
<222> (15)	
<223> D = G, C or A	
<220>	
<223> Description of Artificial Sequence: Synthetic Primer	
<400> 8	
gtytgnggyt trtadat	17
<210> 9	
<211> 30	
<212> DNA	
<213> Homo sapiens	
<400> 9	
tcagagaacc taaaactagt gcacattgtc	30
<210> 10	
<211> 30	
<212> DNA	
<213> Homo sapiens	
<400> 10	
tgccataaga aaaccaccca caagctcaac	30
<210> 11	
<211> 31	
<212> DNA	
<213> Homo sapiens	
<400> 11	
atccgatatac atgctccaga agcccaagag c	31
<210> 12	
<211> 58	
<212> DNA	
<213> Homo sapiens	
<400> 12	

atccctcgag tcacttgcg tcgtcgtct tgttagtcctg gcgtttccgc acaggctg 58

<210> 13
<211> 43
<212> DNA
<213> Homo sapiens

<400> 13
ccccctctaga atagaaggag atatgctcca gaagcccaag agc 43

<210> 14
<211> 52
<212> DNA
<213> Homo sapiens

<400> 14
atccctcgag tcaatgatga tcatgtatgat gctggcggtt ccgcacaggg tg 52

<210> 15
<211> 40
<212> DNA
<213> Homo sapiens

<400> 15
atccctcgag gaaggagata tggaggtgac cggggacgcc 40

<210> 16
<211> 33
<212> DNA
<213> Homo sapiens

<400> 16
agaatactcg agctatgtgg gatcctgtct ggc 33

<210> 17
<211> 30
<212> DNA
<213> Homo sapiens

<400> 17
gacatctcat atgctccaga agcccaagag 30

<210> 18
<211> 30
<212> DNA
<213> Homo sapiens

<400> 18
gtcaggcctc gagcaaagac caggacgtgg

30

<210> 19
<211> 9
<212> PRT
<213> Mus musculus

<400> 19
Glu Val Asp Trp Glu Tyr Phe Tyr Gly
1 5

<210> 20
<211> 9
<212> PRT
<213> Mus musculus

<400> 20
Glu Tyr Phe Tyr Gly Leu Leu Phe Thr
1 5

<210> 21
<211> 6
<212> PRT
<213> Mus musculus

<400> 21
Ile Tyr Lys Pro Gln Thr
1 5

APPENDIX A:
Claims Pending after Preliminary Amendment

91. An isolated DNA fragmentation factor complex for regulating chromatin stability, said complex comprising a DFF40 polypeptide and a DFF45 polypeptide.
94. The complex of claim 91, wherein the DFF40 subunit comprises 20 contiguous amino acids of SEQ ID NO:2.
95. The complex of claim 94, wherein the DFF40 subunit comprises 30 contiguous amino acids of SEQ ID NO:2.
96. The complex of claim 95, wherein the DFF40 subunit comprises 50 contiguous amino acids of SEQ ID NO:2.
97. The complex of claim 96, wherein the DFF40 subunit comprises 100 contiguous amino acids of SEQ ID NO:2.
98. The complex of claim 97, wherein the DFF40 subunit comprises SEQ ID NO:2.
99. The complex of claim 91, wherein the DFF45 subunit comprises 20 contiguous amino acids of SEQ ID NO:4.
100. The complex of claim 99, wherein the DFF45 subunit comprises 30 contiguous amino acids of SEQ ID NO:4.
101. The complex of claim 100, wherein the DFF45 subunit comprises 50 contiguous amino acids of SEQ ID NO:4.
102. The complex of claim 101, wherein the DFF45 subunit comprises 100 contiguous amino acids of SEQ ID NO:4.

103. The complex of claim 102, wherein said DFF45 subunit comprises SEQ ID NO:4.

104. An isolated polypeptide encoding a human DFF40 DNA fragmentation factor.

105. The polypeptide of claim 104, wherein the DNA fragmentation factor comprises 20 contiguous amino acids of SEQ ID NO:2 [check sequence against CAD].

106. The polypeptide of claim 104, wherein the DNA fragmentation factor comprises 30 contiguous amino acids of SEQ ID NO:2.

107. The polypeptide of claim 104, wherein the DNA fragmentation factor comprises 50 contiguous amino acids of SEQ ID NO:2.

108. The polypeptide of claim 104, wherein the DNA fragmentation factor comprises 100 contiguous amino acids of SEQ ID NO:2.

109. The polypeptide of claim 104, wherein the DNA fragmentation factor comprises SEQ ID NO:2.

110. The polypeptide of claim 104, further comprising a second polypeptide.

111. The polypeptide of claim 110, wherein the second polypeptide is an antibody.

112. The polypeptide of claim 110, wherein the second polypeptide comprises a DFF45 fragmentation factor.

113. An isolated peptide having between about 10 and about 100 contiguous amino acids of a human DFF40 DNA fragmentation factor.

114. The peptide of claim 113, wherein the peptide comprises 20 contiguous amino acids of SEQ ID NO:2.
115. The peptide of claim 114, wherein the peptide comprises 30 contiguous amino acids of SEQ ID NO:2.
116. The peptide of claim 113, wherein the peptide is conjugated to a carrier molecule.
117. The peptide of claim 116, wherein the carrier molecule is selected from the group consisting of KLH and BSA.

USPTO-2023-04759